



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/782,257

DATE: 08/31/2004

TIME: 12:22:49

Input Set : N:\Crf3\RULE60\10782257.raw

Output Set: N:\CRF4\08312004\J782257.raw

1 <110> APPLICANT: Biotica Technology Limited  
 2     Leadlay, Peter F  
 3     Pfizer, Inc.  
 4     Staunton, James  
 5     Cortes, Jesus  
 6     McArthur, Hamish AI  
 7 <120> TITLE OF INVENTION: Polyketides and their synthesis  
 8 <130> FILE REFERENCE: IS/CP5787585  
 9 <140> CURRENT APPLICATION NUMBER: US/10/782,257  
 10 <141> CURRENT FILING DATE: 2004-02-19  
 11 <150> PRIOR APPLICATION NUMBER: US/09/720,841  
 12 <151> PRIOR FILING DATE: 2001-08-13  
 13 <150> PRIOR APPLICATION NUMBER: GB 9814006.4  
 14 <151> PRIOR FILING DATE: 1998-06-29  
 15 <160> NUMBER OF SEQ ID NOS: 53  
 16 <170> SOFTWARE: PatentIn Ver. 2.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 398  
 20 <212> TYPE: PRT  
 21 <213> ORGANISM: Streptomyces sp. C5  
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 23     Met Val Thr Gly Leu Gly Ile Val Ala Pro Asn Gly Leu Gly Val Gly  
 24         1                     5                     10                     15  
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 26                     20                     25                     30  
 27     Arg Arg Phe Ala Asp Asp Gly Arg Leu Gly Arg Leu Ala Gly Glu Val  
 28                     35                     40                     45  
 29     Ser Asp Phe Val Pro Glu Asp His Leu Pro Lys Arg Leu Leu Val Gln  
 30         50                     55                     60  
 31     Thr Asp Pro Met Thr Gln Met Thr Ala Leu Ala Ala Ala Glu Trp Ala  
 32         65                     70                     75                     80  
 33     Leu Arg Glu Ala Gly Cys Ala Pro Ser Ser Pro Leu Glu Ala Gly Val  
 34                     85                     90                     95  
 35     Ile Thr Ala Ser Ala Ser Gly Gly Phe Ala Ser Gly Gln Arg Glu Leu  
 36                     100                     105                     110  
 37     Gln Asn Leu Trp Ser Lys Gly Pro Ala His Val Ser Ala Tyr Met Ser  
 38                     115                     120                     125  
 39     Phe Ala Trp Phe Tyr Ala Val Asn Thr Gly Gln Ile Ala Ile Arg His  
 40         130                     135                     140  
 41     Asp Leu Arg Gly Pro Val Gly Val Val Val Ala Glu Gln Ala Gly Gly  
 42         145                     150                     155                     160  
 43     Leu Asp Ala Leu Ala His Ala Arg Arg Lys Val Arg Gly Gly Ala Glu  
 44                     165                     170                     175

ENTERED

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45      Leu Ile Val Ser Gly Ala Met Asp Ser Ser Leu Cys Pro Tyr Gly Met
46              180              185              190
47      Ala Ala Gln Val Arg Ser Gly Arg Leu Ser Gly Ser Asp Asp Pro Thr
48              195              200              205
49      Ala Gly Tyr Leu Pro Phe Asp Arg Arg Ala Ala Gly His Val Pro Gly
50              210              215              220
51      Glu Gly Gly Ala Ile Leu Ala Val Glu Asp Ala Glu Arg Val Ala Glu
52      225              230              235              240
53      Arg Gly Gly Lys Val Tyr Gly Ser Ile Ala Gly Thr Ala Ser Phe Asp
54              245              250              255
55      Pro Pro Pro Gly Ser Gly Arg Pro Ser Ala Leu Ala Arg Ala Val Glu
56              260              265              270
57      Thr Ala Leu Ala Asp Ala Gly Leu Asp Arg Ser Asp Ile Ala Val Val
58              275              280              285
59      Phe Ala Asp Gly Ala Ala Val Gly Glu Leu Asp Val Ala Glu Ala Glu
60      290              295              300
61      Ala Leu Ala Ser Val Phe Gly Pro His Arg Val Pro Val Thr Val Pro
62      305              310              315              320
63      Lys Thr Leu Thr Gly Arg Leu Tyr Ser Gly Ala Gly Pro Leu Asp Val
64              325              330              335
65      Ala Thr Gly Leu Leu Ala Leu Arg Asp Glu Val Val Pro Ala Thr Gly
66              340              345              350
67      His Val His Pro Asp Pro Asp Leu Pro Leu Asp Val Val Thr Gly Arg
68              355              360              365
69      Pro Arg Ala Met Ala Asp Ala Arg Ala Ala Leu Val Val Ala Arg Gly
70      370              375              380
71      His Gly Gly Phe Asn Ser Ala Leu Val Val Arg Gly Ala Ala
72      385              390              395
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 425
76 <212> TYPE: PRT
77 <213> ORGANISM: Streptomyces peucetius
78 <400> SEQUENCE: 2
79      Met Thr Gly Thr Ala Ala Arg Thr Ala Ser Ser Gln Leu His Ala Ser
80              1              5              10              15
81      Pro Ala Gly Arg Arg Gly Leu Arg Gly Arg Ala Val Val Thr Gly Leu
82              20              25              30
83      Gly Ile Val Ala Pro Asn Gly Leu Gly Val Gly Ala Tyr Trp Asp Ala
84              35              40              45
85      Val Leu Asn Gly Arg Asn Gly Ile Gly Pro Leu Arg Arg Phe Thr Gly
86              50              55              60
87      Asp Gly Arg Leu Gly Arg Leu Ala Gly Glu Val Ser Asp Phe Val Pro
88              65              70              75              80
89      Glu Asp His Leu Pro Lys Arg Leu Leu Ala Gln Thr Asp Pro Met Thr
90              85              90              95
91      Gln Tyr Ala Leu Ala Ala Ala Glu Trp Ala Leu Arg Glu Ser Gly Cys
92              100              105              110
93      Ser Pro Ser Ser Pro Leu Glu Ala Gly Val Ile Thr Ala Ser Ala Ser
94              115              120              125

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95 Gly Gly Phe Ala Phe Gly Gln Arg Glu Leu Gln Asn Leu Trp Ser Lys
96      130      135      140
97 Gly Pro Ala His Val Ser Ala Tyr Met Ser Phe Ala Trp Phe Tyr Ala
98      145      150      155      160
99 Val Asn Thr Gly Gln Ile Ala Ile Arg His Asp Leu Arg Gly Pro Val
100      165      170      175
101 Gly Val Val Val Ala Glu Gln Ala Gly Gly Leu Asp Ala Leu Ala His
102      180      185      190
103 Ala Arg Arg Lys Val Arg Gly Gly Ala Glu Leu Ile Val Ser Gly Ala
104      195      200      205
105 Val Asp Ser Ser Leu Cys Pro Tyr Gly Met Ala Ala Gln Val Lys Ser
106      210      215      220
107 Gly Arg Leu Ser Gly Ser Asp Asn Pro Thr Ala Gly Tyr Leu Pro Phe
108      225      230      235      240
109 Asp Arg Arg Ala Ala Gly His Val Pro Gly Glu Gly Gly Ala Ile Leu
110      245      250      255
111 Thr Val Glu Asp Ala Glu Arg Ala Ala Glu Arg Gly Ala Lys Val Tyr
112      260      265      270
113 Gly Ser Ile Ala Gly Tyr Gly Ala Ser Phe Asp Pro Pro Gly Ser
114      275      280      285
115 Gly Arg Pro Ser Ala Leu Ala Arg Ala Val Glu Thr Ala Leu Ala Asp
116      290      295      300
117 Ala Gly Leu Asp Gly Ser Asp Ile Ala Val Val Phe Ala Asp Gly Ala
118      305      310      315      320
119 Ala Val Pro Glu Leu Asp Ala Ala Glu Ala Glu Ala Leu Ala Ser Val
120      325      330      335
121 Phe Gly Pro Arg Arg Val Pro Val Thr Val Pro Lys Thr Leu Thr Gly
122      340      345      350
123 Arg Leu Tyr Ser Gly Ala Gly Pro Leu Asp Val Ala Thr Ala Leu Leu
124      355      360      365
125 Ala Leu Arg Asp Glu Val Val Pro Ala Thr Ala His Val Asp Pro Asp
126      370      375      380
127 Pro Asp Leu Pro Leu Asp Val Val Thr Gly Arg Pro Arg Ser Leu Ala
128      385      390      395      400
129 Asp Ala Arg Ala Ala Leu Leu Val Ala Arg Gly Tyr Gly Gly Phe Asn
130      405      410      415
131 Ser Ala Leu Val Val Arg Gly Ala Ala
132      420      425
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 407
136 <212> TYPE: PRT
137 <213> ORGANISM: Streptomyces coelicolor
138 <400> SEQUENCE: 3
139 Met Ser Val Leu Ile Thr Gly Val Gly Val Val Ala Pro Asn Gly Leu
140      1      5      10      15
141 Gly Leu Ala Pro Tyr Trp Ser Ala Val Leu Asp Gly Arg His Gly Leu
142      20      25      30
143 Gly Pro Val Thr Arg Phe Asp Val Ser Arg Tyr Pro Ala Thr Leu Ala
144      35      40      45

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```

145 Gly Gln Ile Asp Asp Phe His Ala Pro Asp His Ile Pro Gly Arg Leu
146      50                      55                      60
147 Leu Pro Gln Thr Asp Pro Ser Thr Arg Leu Ala Leu Thr Ala Ala Asp
148      65                      70                      75                      80
149 Trp Ala Leu Gln Asp Ala Lys Ala Asp Pro Glu Ser Leu Thr Asp Tyr
150                      85                      90                      95
151 Asp Met Gly Val Val Thr Ala Asn Ala Cys Gly Gly Phe Asp Phe Thr
152                      100                      105                      110
153 His Arg Glu Phe Arg Lys Leu Trp Ser Glu Gly Pro Lys Ser Val Ser
154                      115                      120                      125
155 Val Tyr Glu Ser Phe Ala Trp Phe Tyr Ala Val Asn Thr Gly Gln Ile
156                      130                      135                      140
157 Ser Ile Arg His Gly Met Arg Gly Pro Ser Ser Ala Leu Val Ala Glu
158                      145                      150                      155                      160
159 Gln Ala Gly Gly Leu Asp Ala Leu Gly His Ala Arg Arg Thr Ile Arg
160                      165                      170                      175
161 Arg Gly Thr Pro Leu Val Val Ser Gly Gly Val Asp Ser Ala Leu Asp
162                      180                      185                      190
163 Pro Trp Gly Trp Val Ser Gln Ile Ala Ser Gly Arg Ile Ser Thr Ala
164                      195                      200                      205
165 Thr Asp Pro Asp Arg Ala Tyr Leu Pro Phe Asp Glu Arg Ala Ala Gly
166                      210                      215                      220
167 Tyr Val Pro Gly Glu Gly Gly Ala Ile Leu Val Leu Glu Asp Ser Ala
168                      225                      230                      235                      240
169 Ala Ala Glu Ala Arg Gly Arg His Asp Ala Tyr Gly Glu Leu Ala Gly
170                      245                      250                      255
171 Cys Ala Ser Thr Phe Asp Pro Ala Pro Gly Ser Gly Arg Pro Ala Gly
172                      260                      265                      270
173 Leu Glu Arg Ala Ile Arg Leu Ala Leu Asn Asp Ala Gly Thr Gly Pro
174                      275                      280                      285
175 Glu Asp Val Asp Val Val Phe Ala Asp Gly Ala Gly Val Pro Glu Leu
176                      290                      295                      300
177 Asp Ala Ala Glu Ala Arg Ala Ile Gly Arg Val Phe Gly Arg Glu Gly
178                      305                      310                      315                      320
179 Val Pro Val Thr Val Pro Lys Thr Thr Thr Gly Arg Leu Tyr Ser Gly
180                      325                      330                      335
181 Gly Gly Pro Leu Asp Val Val Thr Ala Leu Met Ser Leu Arg Glu Gly
182                      340                      345                      350
183 Val Ile Ala Pro Thr Ala Gly Val Thr Ser Val Pro Arg Glu Tyr Gly
184                      355                      360                      365
185 Ile Asp Leu Val Leu Gly Glu Pro Arg Ser Thr Ala Pro Arg Thr Ala
186                      370                      375                      380
187 Leu Val Leu Ala Arg Gly Arg Trp Gly Phe Asn Ser Ala Ala Val Leu
188                      385                      390                      395                      400
189 Arg Arg Phe Ala Pro Thr Pro
190                      405
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 403
194 <212> TYPE: PRT

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Input Set : N:\Crif3\RULE60\10782257.raw

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195 &lt;213&gt; ORGANISM: Saccharopolyspora hirsuta

196 &lt;400&gt; SEQUENCE: 4

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197   Met Ser Thr Trp Val Thr Gly Met Gly Val Val Ala Pro Asn Gly Leu
198       1           5           10           15
199   Gly Ala Asp Asp His Trp Ala Ala Thr Leu Lys Gly Arg His Gly Ile
200           20           25           30
201   Ser Arg Leu Ser Arg Phe Asp Pro Thr Gly Tyr Pro Ala Glu Leu Ala
202       35           40           45
203   Gly Gln Val Leu Asp Phe Asp Ala Thr Glu His Leu Pro Lys Arg Leu
204       50           55           60
205   Leu Pro Gln Thr Asp Val Ser Thr Arg Phe Ala Leu Ala Ala Ala Ala
206       65           70           75           80
207   Trp Ala Leu Ala Asp Ala Glu Val Asp Pro Ala Glu Leu Pro Glu Tyr
208           85           90           95
209   Gly Thr Gly Val Ile Thr Ser Asn Ala Thr Gly Gly Phe Glu Phe Thr
210           100          105          110
211   His Arg Glu Phe Arg Lys Leu Trp Ala Gln Gly Pro Glu Phe Val Ser
212           115          120          125
213   Val Tyr Glu Ser Phe Ala Trp Phe Tyr Ala Val Asn Thr Gly Gln Ile
214           130          135          140
215   Ser Ile Arg His Gly Leu Arg Gly Pro Gly Ser Val Leu Val Ala Glu
216       145          150          155          160
217   Gln Ala Gly Gly Leu Asp Ala Val Gly His Gly Gly Ala Val Arg Asn
218           165          170          175
219   Gly Thr Pro Met Val Val Thr Gly Gly Val Asp Ser Ser Phe Asp Pro
220           180          185          190
221   Trp Gly Trp Val Ser His Val Ser Ser Gly Arg Val Ser Arg Ala Thr
222           195          200          205
223   Asp Pro Gly Arg Ala Tyr Leu Pro Phe Asp Val Ala Ala Asn Gly Tyr
224       210          215          220
225   Val Pro Gly Glu Gly Gly Ala Ile Leu Leu Leu Glu Asp Ala Glu Ser
226       225          230          235          240
227   Ala Lys Ala Arg Gly Ala Thr Gly Tyr Gly Glu Ile Ala Gly Tyr Ala
228           245          250          255
229   Ala Thr Phe Asp Pro Ala Pro Gly Ser Glu Arg Pro Pro Ala Leu Arg
230           260          265          270
231   Arg Ala Ile Glu Leu Ala Leu Ala Asp Ala Glu Leu Arg Pro Glu Gln
232           275          280          285
233   Val Asp Val Val Phe Ala Asp Ala Ala Gly Val Ala Glu Leu Asp Ala
234       290          295          300
235   Ile Glu Ala Ala Ala Ile Arg Glu Leu Phe Gly Pro Ser Gly Val Pro
236       305          310          315          320
237   Val Thr Ala Pro Lys Thr Met Thr Gly Arg Leu Tyr Ser Gly Gly Gly
238           325          330          335
239   Pro Leu Asp Leu Val Ala Ala Leu Leu Ala Ile Arg Asp Gly Val Ile
240       340          345          350
241   Pro Pro Thr Val His Thr Ala Glu Pro Val Pro Glu His Gln Leu Asp
242           355          360          365
243   Leu Val Thr Gly Asp Pro Arg His Gln Gln Leu Gly Thr Ala Leu Val

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**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\10782257.raw

Output Set: N:\CRF4\08312004\J782257.raw